

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson

Sequence 1: SEQ_180 252 aa

Sequence 2: G_kaustophilus_deltaprim 328 aa

Start of Pairwise alignments

Aligning...

Sequences (1:2) Aligned. Score: 99

Guide tree file created: [/ebi/extserv/clustalw-

work/interactive/clustalw-20060911-20060223.dnd]

Start of Multiple Alignment

There are 1 groups

Aligning...

Group 1: Sequences: 2 Score:5465

Alignment Score 1571

CLUSTAL-Alignment file created [/ebi/extserv/clustalw-

work/interactive/clustalw-20060911-20060223.aln]

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SEQ_180          MRWEQLAKRQPVVAKMLQSGLEKGRISHAYLFEGQRTGKKAASLLAKR 50
G_kaustophilus_deltaprim MRWEQLAKRQPVVAKMLQSGLEKGRISHAYLFEGQRTGKKAASLLAKR 50
*****

SEQ_180          LFCLSPIGVSPCLECRNCRRIDSGNHDPDVRVIGPDGGSIKKEQIEWLQQE 100
G_kaustophilus_deltaprim LFCLSPIGVSPCLECRNCRRIDSGNHDPDVRVISPDGGSIKKEQIEWLQQE 100
*****

SEQ_180          FSKTAVESDKKMYIVEHADQMTTSAANSLLKFLEEPHPGTVAVLLTEQYH 150
G_kaustophilus_deltaprim FSKTAVESDKKMYIVEHADQMTTSAANSLLKFLEEPHPGTVAVLLTEQYH 150
*****

SEQ_180          RLLGTIVSRCQVLSFRPLPPAELAQGLVEEHVPLPLALLAAHLTNSFEEA 200
G_kaustophilus_deltaprim RLLGTIVSRCQVLSFRPLPPAELAQGLVEEHVPLPLALLAAHLTNSFEEA 200
*****

SEQ_180          LALAKDSWFAEARTLVLQWYEMLGKPELQLLFFIHDRLFPHFLESHQLDL 250
G_kaustophilus_deltaprim LALAKDSWFAEARTLVLQWYEMLGKPELQLLFFIHDRLFPHFLESHQLDL 250
*****

SEQ_180          GL----- 252
G_kaustophilus_deltaprim GLDLLLYLYRDLLHIQAGQMDGVLYRDQLDRLQRWALACPQRRILAGMEA 300
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SEQ_180          -----
G_kaustophilus_deltaprim ILQAKTRLNTTNMSTALLVEQLVLQLKR 328

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